

US 09/991,936

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OIFE #4  
First five pages

<110> APPLICANT: Brandt, Kevin S.  
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Wisniewski, Nancy  
<120> TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE  
NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
<130> FILE REFERENCE: FC-6-C1  
<140> CURRENT APPLICATION NUMBER: 09/991,936  
<141> CURRENT FILING DATE: 2001-11-21  
  
<150> PRIOR APPLICATION NUMBER: US/09/543,668  
<151> PRIOR FILING DATE: 2000-04-07

<150> PRIOR APPLICATION NUMBER: 60/128,704  
<151> PRIOR FILING DATE: 1999-04-09  
<160> NUMBER OF SEQ ID NOS: 1959  
<170> SOFTWARE: PatentIn Ver. 2.1

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<210> SEQ ID NO 1  
<211> LENGTH: 2057  
<212> TYPE: DNA  
<213> ORGANISM: Ctenocephalides felis  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (152)..(1303)  
<400> SEQUENCE: 1

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atctcaagaa gtaatctatt actgaatcaa a atg aaa agc agt acc tgt att 172
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                                Met Lys Ser Ser Thr Cys Ile

ttt ctt ctg gtc att atg ctg aat tgc aag aac ctt gtt aat gct gcg 220
Phe Leu Leu Val Ile Met Leu Asn Cys Lys Asn Leu Val Asn Ala Ala
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tgc acc aac aac gcg cct cca atg aag ata ttc cgt agc cga aga gtt 268
Cys Thr Asn Asn Ala Pro Pro Met Lys Ile Phe Arg Ser Arg Arg Val
      25           30           35
ctt ctc ggt gat ggt act gaa aga gat gct ggc att gta gtt gat tcc 316
Leu Leu Gly Asp Gly Thr Glu Arg Asp Ala Gly Ile Val Val Asp Ser
      40           45           50           55
tcc gga aga ata aaa agt ata att tca gga gaa gaa gtg gaa agg ata 364
Ser Gly Arg Ile Lys Ser Ile Ile Ser Gly Glu Glu Val Glu Arg Ile
      60           65           70
gct aac gaa act aaa gtt gag gtg ttg gac tac ggt caa ttt tca ata 412
Ala Asn Glu Thr Lys Val Glu Val Leu Asp Tyr Gly Gln Phe Ser Ile
      75           80           85
tgg cca ggt gtg ata gac tct cat gtg cac gtc aac gaa cca gga aga 460
Trp Pro Gly Val Ile Asp Ser His Val His Val Asn Glu Pro Gly Arg
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gaa tcc tgg gaa gga tac acc aca gct act aaa gca gca gct tgg ggc 508
Glu Ser Trp Glu Gly Tyr Thr Thr Ala Thr Lys Ala Ala Ala Trp Gly
      105          110          115
ggg att acc aca ata gta gac atg cct ttg aat tcc atc cca cct aca 556
Gly Ile Thr Thr Ile Val Asp Met Pro Leu Asn Ser Ile Pro Pro Thr
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acg cat gtt gat gtc gct ttc tgg gga ggc gtg att cct ggc aat gcg	652
Thr His Val Asp Val Ala Phe Trp Gly Gly Val Ile Pro Gly Asn Ala	
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cac gaa ttg ttg cca ctt atc aac gcc gga gta aga gga ttc aaa tgt	700
His Glu Leu Leu Pro Leu Ile Asn Ala Gly Val Arg Gly Phe Lys Cys	
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Phe Thr Ser Glu Ser Gly Val Asp Glu Phe Pro Gln Val Thr Lys Asn	
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gat ctg gaa atg gct cta aaa gag ctc cag aaa gca aat tcc gta ctt	796
Asp Leu Glu Met Ala Leu Lys Glu Leu Gln Lys Ala Asn Ser Val Leu	
200 205 210 215	
ctg tac cat gcc gaa tta ccc gct cct caa gaa aat gtt aca agc aat	844
Leu Tyr His Ala Glu Leu Pro Ala Pro Gln Glu Asn Val Thr Ser Asn	
220 225 230	
gaa act gaa aag tac atg act tac ctg aaa aca cga cct cca agt atg	892
Glu Thr Glu Lys Tyr Met Thr Tyr Leu Lys Thr Arg Pro Pro Ser Met	
235 240 245	
gaa gta aat gct att gat atg att ata gac ctc aca aaa tat aaa	940
Glu Val Asn Ala Ile Asp Met Ile Ile Asp Leu Thr Lys Lys Tyr Lys	
250 255 260	
gtt agg tct cac ata gtg cat cta tca gca gca ggt gct tta ccg caa	988
Val Arg Ser His Ile Val His Leu Ser Ala Ala Gly Ala Leu Pro Gln	
265 270 275	
ttg aaa aaa gcg cgc tca gag aac gtt cca ctt tcg att gaa act tgt	1036
Leu Lys Lys Ala Arg Ser Glu Asn Val Pro Leu Ser Ile Glu Thr Cys	
280 285 290 295	
cat cat tac tta acc ttt gct gct gaa gat gtt cca gat gga cat act	1084
His His Tyr Leu Thr Phe Ala Ala Glu Asp Val Pro Asp Gly His Thr	
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gaa tac aaa tgc gct cca cca att aga gaa gaa agt aat caa gaa aaa	1132
Glu Tyr Lys Cys Ala Pro Pro Ile Arg Glu Glu Ser Asn Gln Glu Lys	
315 320 325	
tta tgg caa gct ttg gaa aac aga gat att gat atg gta gtc agt gat	1180
Leu Trp Gln Ala Leu Glu Asn Arg Asp Ile Asp Met Val Val Ser Asp	
330 335 340	
cat tct cca tca cct gct gca ctg aaa ggc ctg tgc aat ggt tgt cat	1228
His Ser Pro Ser Pro Ala Ala Leu Lys Gly Leu Cys Asn Gly Cys His	
345 350 355	
cct gat ttc cta aaa gct tgg ggt gga att gct ggt atg cag ttt gga	1276
Pro Asp Phe Leu Lys Ala Trp Gly Gly Ile Ala Gly Met Gln Phe Gly	
360 365 370 375	
tta tct tta ata agg gac cgg tgc ttc taaaagaggc tttaaagctc	1323
Leu Ser Leu Ile Arg Asp Arg Cys Phe	
380	
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cgttgaaggg caaagttcat gcaactgttg tacgaggaga ctttgttttac cgtaatggac	1563
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<211> LENGTH: 384

<212> TYPE: PRT

<213> ORGANISM: Ctenocephalides felis

<400> SEQUENCE: 2

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Ile Phe Arg Ser Arg Arg Val Leu Leu Gly Asp Gly Thr Glu Arg Asp
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Ala Gly Ile Val Val Asp Ser Ser Gly Arg Ile Lys Ser Ile Ile Ser
          50           55           60
Gly Glu Glu Val Glu Arg Ile Ala Asn Glu Thr Lys Val Glu Val Leu
          65           70           75           80
Asp Tyr Gly Gln Phe Ser Ile Trp Pro Gly Val Ile Asp Ser His Val
          85           90           95
His Val Asn Glu Pro Gly Arg Glu Ser Trp Glu Gly Tyr Thr Thr Ala
          100          105          110
Thr Lys Ala Ala Ala Trp Gly Gly Ile Thr Thr Ile Val Asp Met Pro
          115          120          125
Leu Asn Ser Ile Pro Pro Thr Thr Thr Val Glu Asn Leu Arg Thr Lys
          130          135          140
Val Asn Ser Ala Cys Gly Lys Thr His Val Asp Val Ala Phe Trp Gly
          145          150          155          160
Gly Val Ile Pro Gly Asn Ala His Glu Leu Leu Pro Leu Ile Asn Ala
          165          170          175
Gly Val Arg Gly Phe Lys Cys Phe Thr Ser Glu Ser Gly Val Asp Glu
          180          185          190
Phe Pro Gln Val Thr Lys Asn Asp Leu Glu Met Ala Leu Lys Glu Leu
          195          200          205
Gln Lys Ala Asn Ser Val Leu Leu Tyr His Ala Glu Leu Pro Ala Pro
          210          215          220
Gln Glu Asn Val Thr Ser Asn Glu Thr Glu Lys Tyr Met Thr Tyr Leu
          225          230          235          240
Lys Thr Arg Pro Pro Ser Met Glu Val Asn Ala Ile Asp Met Ile Ile
          245          250          255
Asp Leu Thr Lys Lys Tyr Lys Val Arg Ser His Ile Val His Leu Ser
          260          265          270
Ala Ala Gly Ala Leu Pro Gln Leu Lys Lys Ala Arg Ser Glu Asn Val
          275          280          285
Pro Leu Ser Ile Glu Thr Cys His His Tyr Leu Thr Phe Ala Ala Glu
          290          295          300
Asp Val Pro Asp Gly His Thr Glu Tyr Lys Cys Ala Pro Pro Ile Arg
          305          310          315          320
Glu Glu Ser Asn Gln Glu Lys Leu Trp Gln Ala Leu Glu Asn Arg Asp
          325          330          335
Ile Asp Met Val Val Ser Asp His Ser Pro Ser Pro Ala Ala Leu Lys
          340          345          350
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&lt;210&gt; SEQ ID NO 3

&lt;211&gt; LENGTH: 2057

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Ctenocephalides felis

&lt;400&gt; SEQUENCE: 3

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gaagtttggt cgggttaattt tcaggcagag gtgctattg tagtaataaa acaattttta 420
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taatcatatc aatagcattt acttccatac ttggagggtcg tgttttcagg taagtcatgt 1200
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&lt;210&gt; SEQ ID NO 4

&lt;211&gt; LENGTH: 1152

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Ctenocephalides felis

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(1152)

&lt;400&gt; SEQUENCE: 4

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Lys Asn Leu Val Asn Ala Ala Cys Thr Asn Asn Ala Pro Pro Met Lys
20 25 30

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35 40 45	
gct ggc att gta gtt gat tcc gga aga ata aaa agt ata att tca	192
Ala Gly Ile Val Val Asp Ser Ser Gly Arg Ile Lys Ser Ile Ile Ser	
50 55 60	
gga gaa gaa gtg gaa agg ata gct aac gaa act aaa gtt gag gtg ttg	240
Gly Glu Glu Val Glu Arg Ile Ala Asn Glu Thr Lys Val Glu Val Leu	
65 70 75 80	
gac tac ggt caa ttt tca ata tgg cca ggt gtg ata gac tct cat gtg	288
Asp Tyr Gly Gln Phe Ser Ile Trp Pro Gly Val Ile Asp Ser His Val	
85 90 95	
cac gtc aac gaa cca gga aga gaa tcc tgg gaa gga tac acc aca gct	336
His Val Asn Glu Pro Gly Arg Glu Ser Trp Glu Gly Tyr Thr Thr Ala	
100 105 110	
act aaa gca gca gct tgg ggc ggg att acc aca ata gta gac atg cct	384
Thr Lys Ala Ala Ala Trp Gly Gly Ile Thr Thr Ile Val Asp Met Pro	
115 120 125	
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Val Asn Ser Ala Cys Gly Lys Thr His Val Asp Val Ala Phe Trp Gly	
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Gly Val Ile Pro Gly Asn Ala His Glu Leu Leu Pro Leu Ile Asn Ala	
165 170 175	
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Gly Val Arg Gly Phe Lys Cys Phe Thr Ser Glu Ser Gly Val Asp Glu	
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Phe Pro Gln Val Thr Lys Asn Asp Leu Glu Met Ala Leu Lys Glu Leu	
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cag aaa gca aat tcc gta ctt ctg tac cat gcc gaa tta ccc gct cct	672
Gln Lys Ala Asn Ser Val Leu Leu Tyr His Ala Glu Leu Pro Ala Pro	
210 215 220	
caa gaa aat gtt aca agc aat gaa act gaa aag tac atg act tac ctg	720
Gln Glu Asn Val Thr Ser Asn Glu Thr Glu Lys Tyr Met Thr Tyr Leu	
225 230 235 240	
aaa aca cga cct cca agt atg gaa gta aat gct att gat atg att ata	768
Lys Thr Arg Pro Pro Ser Met Glu Val Asn Ala Ile Asp Met Ile Ile	
245 250 255	
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Asp Leu Thr Lys Lys Tyr Lys Val Arg Ser His Ile Val His Leu Ser	
260 265 270	
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Asp Val Pro Asp Gly His Thr Glu Tyr Lys Cys Ala Pro Pro Ile Arg	
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